FY16 USWBSI PROJECT ABSTRACT

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PROJECT 2 ABSTRACT

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Screening for FHB resistance in barley is laborious, resource intensive, and vulnerable to unpredictable environmental conditions in the field. Previous genetic studies using bi-parental mapping populations and association mapping indicate that FHB resistance is controlled by many moderate effect and small effect QTL that co-segregate with important traits such as heading date, spike morphology, and grain protein concentration (Canci et al., 2003; Horsley et al., 2006; Mesfin et al., 2003; Nduulu et al., 2007; Massman et al, 2011).

Genomic selection (GS) is a marker-based breeding method that combines genome-wide marker data with phenotypes to produce predictions on performance, which is the best approach for complex traits such as FHB resistance. The appeal of GS has dramatically increased as the cost of genome-wide marker data has approached that of phenotyping. Studies on GS using cross validation (Lorenz et al., 2012) progeny performance prediction (Lorenz and Smith, 2015) have indicated GS holds promise as an alternative breeding strategy for barley FHB resistance. Moreover, GS holds fantastic potential to identify promising crosses superior in mean performance as well as progeny variance, and thus improve potential for identifying transgressive segregates (Mohammadi et al., 2015).

The UMN Barley Breeding program initiated a GS program for FHB resistance in the fall of 2009. Since then, five cycles of genomic selection have been conducted. In addition to the phenotypic and genotypic data collected on progenies from the five cycles of selection, pheno/genotypic data has been collected on several other populations through the T-CAP, including two-row barley populations. There are numerous variables that can be manipulated in a GS breeding scheme to optimize prediction accuracy and choice of parent combinations including: number, distribution, and imputation of markers; size and composition of the training population; and type of environments used to create the training data sets (Lorenz et al., 2011; Heslot et al., 2015). Investigating the effect of manipulating GS parameters on accuracy and the potential of using genomic prediction to identify crosses more likely to produce transgressive segregates will allow us to optimize the use of GS in breeding for FHB resistance.
Our objectives are to 1) Characterize the effects of GS parameters on prediction accuracy and the identification of superior crosses, where a superior cross is one with high progeny mean and variance; 2) Contribute to the optimization of GS through better training population design.